

# SCORE Search Results Details for Application 10828332 and Search Result us-10-828-332-6.rnpm.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
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This page gives you Search Results detail for the Application 10828332 and Search Result us-10-828-332-6.rnpm.

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2006, 03:25:21 ; Search time 10101 Seconds  
(without alignments)  
9606.645 Million cell updates/sec

Title: US-10-828-332-6  
Perfect score: 1755  
Sequence: 1 atgccaggggtatcatcatc.....acaccaaccatgccatctag 1755

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_Main:\*

- 1: /cgn2\_6/ptodata/1/pna/PCTUSA\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pna/PCTUSB\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pna/PCTUSC\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pna/US06\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pna/US075\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pna/US076\_COMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pna/US077\_COMB.seq:\*
- 8: /cgn2\_6/ptodata/1/pna/US078\_COMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pna/US079\_COMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pna/US080\_COMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pna/US082\_COMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pna/US083\_COMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pna/US084\_COMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pna/US085\_COMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pna/US086\_COMB.seq:\*

# SCORE Search Results Details for Application 10828332 and Search Result us-10-828-332- 6.rnpn.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
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This page gives you Search Results detail for the Application 10828332 and Search Result us-10-828-332-6.rnpn.

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2006, 03:27:02 ; Search time 722 Seconds  
(without alignments)  
7897.181 Million cell updates/sec

Title: US-10-828-332-6  
Perfect score: 1755  
Sequence: 1 atgccaggggtatcatcatc.....acaccaaccatgccatctag 1755

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7549803 seqs, 1624434298 residues

Total number of hits satisfying chosen parameters: 15099606

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*

- 1: /SIDS5/ptodata/1/pna/PCT\_NEW\_COMB.seq:\*
- 2: /SIDS5/ptodata/1/pna/US06\_NEW\_COMB.seq:\*
- 3: /SIDS5/ptodata/1/pna/US07\_NEW\_COMB.seq:\*
- 4: /SIDS5/ptodata/1/pna/US08\_NEW\_COMB.seq:\*
- 5: /SIDS5/ptodata/1/pna/US09\_NEW\_COMB.seq:\*
- 6: /SIDS5/ptodata/1/pna/US10\_NEW\_COMB.seq:\*
- 7: /SIDS5/ptodata/1/pna/US10\_NEW\_COMB.seq1:\*
- 8: /SIDS5/ptodata/1/pna/US11\_NEW\_COMB.seq:\*
- 9: /SIDS5/ptodata/1/pna/US11\_NEW\_COMB.seq1:\*
- 10: /SIDS5/ptodata/1/pna/US11\_NEW\_COMB.seq2:\*
- 11: /SIDS5/ptodata/1/pna/US11\_NEW\_COMB.seq3:\*
- 12: /SIDS5/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	3	gabriel near ana	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 09:04
L2	1	gabriel near san near ana	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 08:44
L3	1809	gabriel near san	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 08:44
L4	6	maekawa near takami	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 09:04
L5	14	uneyama near hisayuki	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 09:05
L6	17	l1 or l2 or l4 or l5	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 09:05
L7	6	l6 and glutamic	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 09:08
L8	5029	glutamic adj acid.clm.	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 09:08
L9	390	l8 and receptor.clm.	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 09:10
L10	14	l9 and metabotrop\$3	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 09:10

=> d his

(FILE 'HOME' ENTERED AT 09:13:08 ON 02 OCT 2006)

FILE 'MEDLINE, CAPLUS, BIOSIS' ENTERED AT 09:13:26 ON 02 OCT 2006

L1 20033 S METABOTROP?  
L2 18304 S L1 (P) GLUTAM?  
L3 18203 S L2 (P) RECEPTOR  
L4 0 S L3 AND GABRIEL  
L5 17057 S L3 AND GLUTAMATE (1W) RECEPTOR  
L6 17003 S L5 AND METABOTROPIC  
L7 9227 DUP REM L6 (7776 DUPLICATES REMOVED)  
L8 0 S L7 AND PU<2000  
L9 4049 S L7 AND PY<2000  
L10 2654 S L9 AND PY>1995  
L11 743 S L10 AND PY>1998  
L12 0 S L11 AND SEQ NEAR ID  
L13 67 S L11 AND SEQUENCE  
L14 10 S L13 AND MRNA  
E GABRIEL ANA S /AU  
E GABRIEL SAN /AU  
E MAEKAWA TAKAMI /AU  
E UNEYAMA HISAYUKI /AU  
L15 14284 S E 3  
E MAEKAWA TAKAMI /AU  
L16 17 S E3  
L17 1 S L16 AND GLUTAMIC

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: April 25, 2006, 12:46:23 ; Search time 160.3 Seconds  
(without alignments)  
3025.990 Million cell updates/sec

Title: US-10-828-332-6  
Perfect score: 3303  
Sequence: 1 atgccaggggtatcatcatc.....acaccaaccatgccatctag 1755

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 15722378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_n2p.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10828332/runat\_25042006\_092247\_27363/app\_query.fasta\_1  
-DB=Pending\_Patents\_AA\_Main -QFMT=fastan -SUFFIX=rapm -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abss02p -USER=US10828332\_@CGN\_1\_1\_1104\_@runat\_25042006\_092247\_27363  
-NCPU=6 -ICPU=3 -NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending\_Patents\_AA\_Main:\*  
1: /cgn2\_6/ptodata/1/paa/PCTUS\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/paa/US066\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US073\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US074\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US075\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US076\_COMB.pep:\*  
7: /cgn2\_6/ptodata/1/paa/US077\_COMB.pep:\*  
8: /cgn2\_6/ptodata/1/paa/US078\_COMB.pep:\*  
9: /cgn2\_6/ptodata/1/paa/US079\_COMB.pep:\*  
10: /cgn2\_6/ptodata/1/paa/US080\_COMB.pep:\*  
11: /cgn2\_6/ptodata/1/paa/US081\_COMB.pep:\*  
12: /cgn2\_6/ptodata/1/paa/US082\_COMB.pep:\*

13: /cgn2\_6/ptodata/1/paa/US083\_COMB.pep:\*  
 14: /cgn2\_6/ptodata/1/paa/US084\_COMB.pep:\*  
 15: /cgn2\_6/ptodata/1/paa/US085\_COMB.pep:\*  
 16: /cgn2\_6/ptodata/1/paa/US086\_COMB.pep:\*  
 17: /cgn2\_6/ptodata/1/paa/US087\_COMB.pep:\*  
 18: /cgn2\_6/ptodata/1/paa/US088\_COMB.pep:\*  
 19: /cgn2\_6/ptodata/1/paa/US089\_COMB.pep:\*  
 20: /cgn2\_6/ptodata/1/paa/US090\_COMB.pep:\*  
 21: /cgn2\_6/ptodata/1/paa/US091\_COMB.pep:\*  
 22: /cgn2\_6/ptodata/1/paa/US092\_COMB.pep:\*  
 23: /cgn2\_6/ptodata/1/paa/US093\_COMB.pep:\*  
 24: /cgn2\_6/ptodata/1/paa/US094\_COMB.pep:\*  
 25: /cgn2\_6/ptodata/1/paa/US095\_COMB.pep:\*  
 26: /cgn2\_6/ptodata/1/paa/US096\_COMB.pep:\*  
 27: /cgn2\_6/ptodata/1/paa/US097\_COMB.pep:\*  
 28: /cgn2\_6/ptodata/1/paa/US098\_COMB.pep:\*  
 29: /cgn2\_6/ptodata/1/paa/US099\_COMB.pep:\*  
 30: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep:\*  
 31: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep:\*  
 32: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep:\*  
 33: /cgn2\_6/ptodata/1/paa/US103\_COMB.pep:\*  
 34: /cgn2\_6/ptodata/1/paa/US104\_COMB.pep:\*  
 35: /cgn2\_6/ptodata/1/paa/US105\_COMB.pep:\*  
 36: /cgn2\_6/ptodata/1/paa/US106\_COMB.pep:\*  
 37: /cgn2\_6/ptodata/1/paa/US107\_COMB.pep:\*  
 38: /cgn2\_6/ptodata/1/paa/US108\_COMB.pep:\*  
 39: /cgn2\_6/ptodata/1/paa/US109\_COMB.pep:\*  
 40: /cgn2\_6/ptodata/1/paa/US110\_COMB.pep:\*  
 41: /cgn2\_6/ptodata/1/paa/US111\_COMB.pep:\*  
 42: /cgn2\_6/ptodata/1/paa/US112\_COMB.pep:\*  
 43: /cgn2\_6/ptodata/1/paa/US114\_COMB.pep:\*  
 44: /cgn2\_6/ptodata/1/paa/US600\_COMB.pep:\*  
 45: /cgn2\_6/ptodata/1/paa/US601\_COMB.pep:\*  
 46: /cgn2\_6/ptodata/1/paa/US602\_COMB.pep:\*  
 47: /cgn2\_6/ptodata/1/paa/US603\_COMB.pep:\*  
 48: /cgn2\_6/ptodata/1/paa/US604\_COMB.pep:\*  
 49: /cgn2\_6/ptodata/1/paa/US605\_COMB.pep:\*  
 50: /cgn2\_6/ptodata/1/paa/US606\_COMB.pep:\*  
 51: /cgn2\_6/ptodata/1/paa/US607\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	3107	94.1	584	38	US-10-828-332-7	Sequence 7, Appli
2	3050.5	92.4	912	32	US-10-219-051B-4035	Sequence 4035, Ap
3	3050.5	92.4	912	32	US-10-219-051B-4039	Sequence 4039, Ap
4	3004.5	91.0	704	39	US-10-932-333-1999	Sequence 1999, Ap
5	3004.5	91.0	704	49	US-60-500-315-1999	Sequence 1999, Ap
6	3004.5	91.0	909	26	US-09-679-664-48	Sequence 48, Appl
7	3004.5	91.0	912	1	PCT-US04-00750-66	Sequence 66, Appl
8	3004.5	91.0	912	18	US-08-816-178A-2	Sequence 2, Appli

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: April 25, 2006, 12:46:47 ; Search time 20.5 Seconds  
(without alignments)  
2553.097 Million cell updates/sec

Title: US-10-828-332-6  
Perfect score: 3303  
Sequence: 1 atgccaggggtatcatcatc.....acaccaaccatgccatctag 1755

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 629085 seqs, 149112515 residues

Total number of hits satisfying chosen parameters: 1258170

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_n2p.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10828332/runat\_25042006\_092249\_27375/app\_query.fasta\_1  
-DB=Pending\_Patents\_AA\_New -QFMT=fastan -SUFFIX=rapn -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abss02p -USER=US10828332\_@CGN\_1\_1\_107\_@runat\_25042006\_092249\_27375  
-NCPU=6 -ICPU=3 -NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending\_Patents\_AA\_New:\*  
1: /SIDS5/ptodata/1/paa/PCT\_NEW\_COMB.pep:\*  
2: /SIDS5/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /SIDS5/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /SIDS5/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /SIDS5/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /SIDS5/ptodata/1/paa/US10\_NEW\_COMB.pep:\*  
7: /SIDS5/ptodata/1/paa/US11\_NEW\_COMB.pep:\*  
8: /SIDS5/ptodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	%				ID	Description
	No.	Score	Match	Length DB		
	1	2219	67.2	915	8 US-60-732-162-1552	Sequence 1552, Ap
	2	2210	66.9	915	6 US-11-344-728-2	Sequence 2, Appli
	3	2191.5	66.3	922	8 US-60-732-162-1554	Sequence 1554, Ap
	4	2189	66.3	913	8 US-60-732-162-1556	Sequence 1556, Ap
	5	2054	62.2	877	6 US-11-214-063A-1132	Sequence 1132, Ap
	6	1284.5	38.9	1520	6 US-11-214-063A-630	Sequence 630, App
	7	1283	38.8	364	6 US-11-293-697-4612	Sequence 4612, Ap
	8	1131	34.2	1194	6 US-10-567-867-636	Sequence 636, App
	9	1131	34.2	1194	8 US-60-751-420-1596	Sequence 1596, Ap
	10	1123	34.0	1180	1 PCT-US06-13172-7	Sequence 7, Appli
	11	1123	34.0	1180	8 US-60-742-219-2500	Sequence 2500, Ap
	12	1121.5	34.0	878	7 US-11-404-939-347	Sequence 347, App
	13	1113	33.7	1199	6 US-11-271-139-2	Sequence 2, Appli
c	14	873	26.4	297	6 US-10-498-451-1262	Sequence 1262, Ap
	15	528	16.0	297	7 US-11-360-355-120729	Sequence 120729,
	16	521	15.8	684	7 US-11-360-355-120999	Sequence 120999,
	17	428.5	13.0	839	8 US-60-751-420-42	Sequence 42, Appl
	18	427.5	12.9	879	6 US-11-214-063A-454	Sequence 454, App
	19	426.5	12.9	929	6 US-11-214-063A-868	Sequence 868, App
	20	359.5	10.9	936	6 US-11-214-063A-602	Sequence 602, App
	21	313.5	9.5	371	7 US-11-360-355-120501	Sequence 120501,
	22	299	9.1	4315	6 US-10-461-673-9612	Sequence 9612, Ap
	23	282.5	8.6	595	8 US-60-742-219-2100	Sequence 2100, Ap
	24	282.5	8.6	755	6 US-11-214-063A-450	Sequence 450, App
	25	277.5	8.4	413	7 US-11-056-355B-4735	Sequence 4735, Ap
	26	271	8.2	7285	6 US-11-272-521-28	Sequence 28, Appl
	27	265	8.0	493	7 US-11-056-355B-65494	Sequence 65494, A
	28	262	7.9	375	7 US-11-056-355B-3621	Sequence 3621, Ap
	29	261.5	7.9	519	7 US-11-056-355B-6752	Sequence 6752, Ap
	30	259.5	7.9	487	7 US-11-056-355B-6753	Sequence 6753, Ap
	31	258.5	7.8	3682	7 US-11-174-307B-2486	Sequence 2486, Ap
	32	251.5	7.6	2757	7 US-11-174-307B-1642	Sequence 1642, Ap
	33	249.5	7.6	502	6 US-10-461-673-12610	Sequence 12610, A
	34	247	7.5	4440	6 US-10-184-614A-525	Sequence 525, App
	35	247	7.5	4440	6 US-10-184-615A-525	Sequence 525, App
	36	245.5	7.4	1659	7 US-11-174-307B-3184	Sequence 3184, Ap
	37	243	7.4	2118	6 US-11-192-046-125	Sequence 125, App
	38	243	7.4	2578	6 US-10-244-081A-31	Sequence 31, Appl
	39	242.5	7.3	1269	7 US-11-174-307B-164	Sequence 164, App
	40	242.5	7.3	1356	7 US-11-174-307B-64	Sequence 64, Appl
	41	242	7.3	291	7 US-11-056-355B-3800	Sequence 3800, Ap
	42	241.5	7.3	3259	7 US-11-174-307B-1020	Sequence 1020, Ap
	43	241.5	7.3	3259	7 US-11-174-307B-2622	Sequence 2622, Ap
	44	241.5	7.3	4243	7 US-11-174-307B-1722	Sequence 1722, Ap
	45	241	7.3	473	1 PCT-US06-07136-166	Sequence 166, App

## ALIGNMENTS

RESULT 1  
US-60-732-162-1552